

## SEQUENCE LISTING

<110> BANYU PHARMACEUTICAL CO., LTD.

<120> NOVEL GUANOSINE TRIPHOSPHATE (GTP) BINDING PROTEIN-COUPLED RECEPTOR  
PROTEINS

<130> B1-103PCT

<140>

<141>

<150> PCT/JP98/05967

<151> 1998-12-25

<150> JP 1999-145661

<151> 1999-05-25

<160> 26

<170> PatentIn Ver. 2.0

<210> 1

<211> 413

<212> PRT

<213> Rattus norvegicus

<400> 1

Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu

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Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala

20 25 30

Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr

35 40 45

Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser

50 55 60

Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp

65 70 75 80

Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu

85 90 95

Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val

100 105 110

Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile

115

120

125

Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala

130

135

140

Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp

145

150

155

160

Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr

165

170

175

Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe

180

185

190

Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe

195

200

205

Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn

210

215

220

Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly

225

230

235

240

Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro

245

250

255

Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu

260

265

270

His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu

275

280

285

Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg

290

295

300

Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg

305

310

315

320

Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly

325

330

335

Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys

340

345

350

His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu

355

360

365

Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His

370

375

380

Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu

385

390

395

400

410

〈213〉 *Rattus norvegicus*

 $\langle 222 \rangle \quad (1) \dots (1239)$ 

1                      5                      10                      15

20 25 30

35                      40                      45

Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser

60

Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp

80

Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu

95

Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val

110

Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile

125

Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala

140

cag cag ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg 480

cca gaa ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc 768  
Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro  
245 250 255

270

285

300

320

335

350

cat ggc cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt 1104



His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu

355

360

365

ctg tgg gcc aac tgc gcc gtc aac ccc gtc ctc tac cca ctg tgc cac 1152

Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His

370

375

380

tac agc ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc 1200

Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu

385

390

395

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aag gtc cag ccc cac gcc tcc ctg gag cag tgc tgg aag 1239

Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys

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<210> 3

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificially  
synthesized primer sequence

<400> 3

baingccaac ctbkctttct c

<210> 4

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificially  
synthesized primer sequence

<400> 4

ccataaaagn nggggttgac

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<210> 5

<211> 2700

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (351)..(1589)

<400> 5

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accgacgcac cgcgggcggc tggagctcgg ctttgccttc gctgcagcag ccgcgccgcc 120

cgccccactc cgctcagatt ccgacaccag cccctcttgg atcgccctcc tggactctag 180

cccgggctct tgcctcgacc ccgcggacca tgctccgggc gccccccgga aaaccgggct 240

gggcgaagag ccggcaaaga ttaggctcac gagcgggggc cccacccggc caccagctc 300

tccgcccgtg ccttgcccgg tgtccccgag ccgigtgagc ctgctgggcc atg gag 356

Met Glu

1

cgc gcg ccg ccc gac ggg ctg atg aac gcg tcg ggc act ctg gcc gga 404

Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu Ala Gly

5

10

15

gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc tgg acc 452

Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala Trp Thr

20

25

30

gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca gta ctg 500

Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr Val Leu

35

40

45

50

ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc ctc cgc 548

Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser Leu Arg

55

60

65

T05390-630700

acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac ttc ctc 596

Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp Phe Leu

70

75

80

gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg acc ggc 644

Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu Thr Gly

85

90

95

cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg gta gac 692

Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val Val Asp

100

105

110

tac cta ctg tgt gcc tcc tgc gtc ttc aac atc gta ctc atc agc tat 740

Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile Ser Tyr

115

120

125

130

gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc cag cag 788

Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala Gln Gln

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140

145

ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg gtg ctg 836

Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp Val Leu

150

155

160

gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac ctg tct 884

T0390-EST-0000

Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr Leu Ser

165

170

175

ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc ttc tac 932

Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe Phe Tyr

180

185

190

aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc acg ccc 980

Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe Thr Pro

195

200

205

210

ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac atc cag 1028

Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn Ile Gln

215

220

225

agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc cca gaa 1076

Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly Pro Glu

230

235

240

ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc agc tgc 1124

Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro Ser Cys

245

250

255

tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg cac agc 1172

Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu His Ser

260

265

270

gcc aac tcg gcc gtc aac ccc gtc ctc tac cca ctg tgc cac tac agc 1508

Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His Tyr Ser

375

380

385

ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc aag gtc 1556

Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu Lys Val

390

395

400

cag ccc cac ggc tcc ctg gag cag tgc tgg aag tgagcagctg cccaccctt 1609

Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys

405

410

ctgaggccag gcccttgtac tigtltgagi gggcagccgg agcgtgggcg gggcccttgt 1669

ccaigtctcg cicc aaatgc catggcggcc tcttagatca tcaaccccg c agtggggtag 1729

catggcaggt gggccaagag ccctagtggg tggagctaga gtgtgtctgt tagctctgcc 1789

gccacattct ccttcaccac acagaagaga caatccagga gtcccaggca tgccttccac 1849

ctacacacac acacacacac acacacacac acacaccaca gtcagtgcc agtgaigtcc 1909

ccttttgcat atttagtgtt tgggtgtctc cctaagtcaa acctcggtgt gtgtctccgg 1969

ctccggccct ggcaatgcgt gcgtgcgccc tgcattgtgt cacaccgcc acacaccgc 2029

cgcacacaca ctgcaaac ctcctctctc ccagaagagc tggggacgat gcccttgtct 2089

gccactgtct ctigtctaat cccagagcct ggctccttat cccccactct ccttcaact 2149  
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 aaaaaaaaaa a 2700

<210> 6

<211> 29



<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially  
synthesized primer sequence

<400> 6

cgaggatccg tgaggctccg gggcccgtc

29

<210> 7

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially  
synthesized primer sequence

<400> 7

cgggtaagct tcacgacacc tgaaatggaa ga

32

<210> 8

<211> 24

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

ccttctgcat cccattgtac gtacc

$\langle 211 \rangle$  21

$\langle 212 \rangle$  DNA

### <213> Artificial Sequence

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

cttcgccgg gccitacca a

21

 $\langle 210 \rangle$  10

&lt;211&gt; 24

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### <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially  
synthesized primer sequence

<400> 10

acagacacgg cggggctcac

20

<210> 11

<211> 1350

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (280)..(557)

<400> 11

gcactcggct gcgcgttgcn tccggctgca cggtcgcacc ggcagcggct caggctccgg 60

ctctctctcc gctgcagcag ccgcgctgcc ggccccactg ggctcggatc cggccccggc 120

ccccctggca ccgcctgctc tggccccggc cccggccccg cggaccaatgc gctgggcgcc 180

cccaggggaa cccgacccgg ccaagggcc gcaaagacga ggctcccggg ccggggcccc 240

tcccgccgc ccagctctcg gccggcgccc tgccccgcgt cccggagccg cgtgagcctg 300

caggctctgc tgccggctgg ggggcggggc acgcggaggg ggctggagcg ccagacacct 1080

gttggggctg tgaggctcgt ctcccagacg ctccaagccc gcttggcagt agtagtagcg 1140

gctggcggct ggccggctgca accaagtgcc ctctcagcca ggagaaagge ttctccttg 1200

tctaagctga gaccgagggc tctccagcgc cagggtaggg gctggagtcc agcgggggag 1260

gggagaagga aatigtcttc ttctctctt tgagggtcgg gagggctgga cagaagtgca 1320

gggaatcccg atccaggct ctgggggtc 1350

<210> 12

<211> 448

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (259)..(425)

<400> 12

gagctcccca tgcttgatc atccctctcgt cccccaggcc caggggacac agatagtgt 60

gggagctatg tgggggtgaa ggctggcggc agggcagagt ttgtggctga caccaggtgg 120

TGAGGCTCCTG

1

240

300

360

420

448

<213> Homo sapiens

$\langle 222 \rangle$  (293) .. (1209)

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120

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cccagcccaa tatccctcc gcccggccc tgaccagct gccctctgc aggtctcata 300

ccggggccag cagggtgaca cgcggcgggc agtgcggaag atgctgctgg tgggggtgct 360

ggccttccg ctgtacggac cagccatct gagctgggag tactgtccg ggggcagctc 420

catccccgag ggccactgct atcccgagtt ctctacaac tggctacttc tcatcacggc 480

ttccacctg gagtcttta cgccttctt cagctcacc ttcttiaacc tcagcatcta 540

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cgagccccc cccgaggccc agccctcacc acccccacc cctggctgct ggggctgctg 660

gcagaagggg cagggggagg ccatgccgt gcacaggtat ggggtgggtg aggcggccgt 720

aggcgtgag gccggggagg cgacctcgg ggggtggcgt gggggcggct ccgtggcttc 780

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ggccaactcg gctgtcaacc ctgtcctcta cctctgtgc caccacagct tccgccgggc 1140

cttcaccaag ctgctctgcc ccagaagct caaaatccag cccacagct cctggagca 1200

ctgctggaag tgagtggccc accagagcct cctcagcca cgctctctc agcccaggtc 1260

tctggggcat ctggccctgc tggcccttac ccggctcgtt ccccagggg tgagccccgc 1320

cgctctgtg gccctctctt aatgccacgg cagccacctt gccatggagg cgcttccctg 1380

ggttggccag agggccctc actggctgga ctggaggctg ggtggccggc cctgcccccc 1440

acattctggc tccaccggga gggacagctt ggaggicca gacatgctgc ccacccctg 1500

ctggtgcca ccttcgcag ttactggttg gtgttcttc caaagcaagc acctgggtgt 1560

gtccaggct tctgcccata gcagtgtgcc tctgcacgtg cacacacctg cacacccctg 1620

cacacacctg cacaccgtc ctctccccg acaagcccag gacactgctt ttgtgcctt 1680



ctgtctcttg cataagcctc aggcctggcc ctttaccce tcttcccacc aactctctct 1740

gcccccaaaa gtgtcaaggg gccctaggaa cctcgaagct gtctcttgct tttccattct 1800

gggtgttttc agaaagatga agaagaaaac atgctgtga acttgatgtt cctgggaigt 1860

ttaatcaaga gagacaaaat tgctgaggag ctc 1893

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially  
synthesized primer sequence

<400> 14

tgaacgcttc gggggcgctg 20

<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially  
synthesized primer sequence

<400> 15

gagatggcga ggttgagcag g

21

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially  
synthesized primer sequence

<400> 16

ggctccaage catcggcgtc

20

<210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially

synthesized primer sequence

<400> 17

ctcacitcca gcagtgtccc

20

<210> 18

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially  
synthesized primer sequence

<400> 18

gcctccgcac ccagaacaac

20

<210> 19

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially  
synthesized primer sequence

TO3390-250T5350

&lt;400&gt; 19

tgcgcctctg gatgttcag

19

&lt;210&gt; 20

&lt;211&gt; 453

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 20

Met Glu Arg Ala Pro Pro Asp Gly Pro Leu Asn Ala Ser Gly Ala Leu

1

5

10

15

Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala

20

25

30

Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr

35

40

45

Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser

50

55

60

Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp

65

70

75

80

Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu

85

90

95

T0530:EST0600

Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val

100

105

110

Val Asp Tyr Leu Leu Cys Thr Ser Ser Ala Phe Asn Ile Val Leu Ile

115

120

125

Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala

130

135

140

Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Leu Leu Val Trp

145

150

155

160

Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr

165

170

175

Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe

180

185

190

Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe

195

200

205

Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn

210

215

220

Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Ala Arg Glu Ala Ala

355                      360                      365

Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys

370

375

380

His Gly His Cys Val Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu

385

390

395

400

Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His

405

410

415

His Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu

420

425

430

Lys Ile Gln Pro His Ser Ser Leu Glu His Cys Trp Lys Lys Met Lys

435

440

445

Lys Lys Thr Cys Leu

450

<210> 21

<211> 2050

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (271)..(1629)

agagatgtag ggcgccccctt ttagctgcgc acagaacgaa agaactcgtt ttttcttttaa 60

aggctgcgga ggcagagctg catgctgggt gcgggaagag gtgggctccg tcgcggagtc 180

actcccggag ccgcgtgagc ctcgggggcc atg gag cgc gcg ccg ccc gac ggg 294

1

5

Pro Leu Asn Ala Ser Gly Ala Leu Ala Gly Glu Ala Ala Ala Ala Gly

10

15

20

Gly Ala Arg Gly Phe Ser Ala Ala Trp Thr Ala Val Leu Ala Ala Leu

25

30

35

40

Met Ala Leu Leu Ile Val Ala Thr Val Leu Gly Asn Ala Leu Val Met

45

50

55



ctc gcc ttc gtg gcc gac tcg agc ctc cgc acc cag aac aac ttc ttc 486  
 Leu Ala Phe Val Ala Asp Ser Ser Leu Arg Thr Gln Asn Asn Phe Phe  
 60 65 70

ctg ctc aac ctc gcc atc tcc gac ttc ctc gtc ggc gcc ttc tgc atc 534  
 Leu Leu Asn Leu Ala Ile Ser Asp Phe Leu Val Gly Ala Phe Cys Ile  
 75 80 85

cca ctg tat gta ccc tac gtg ctg aca ggc cgc tgg acc ttc ggc cgc 582  
 Pro Leu Tyr Val Pro Tyr Val Leu Thr Gly Arg Trp Thr Phe Gly Arg  
 90 95 100

ggc ctc tgc aag ctg tgg ctg gta gtg gac tac ctg ctg tgc acc tcc 630  
 Gly Leu Cys Lys Leu Trp Leu Val Val Asp Tyr Leu Leu Cys Thr Ser  
 105 110 115 120

tct gcc ttc aac atc gtg ctc atc agc tac gac cgc ttc ctg tcg gtc 678  
 Ser Ala Phe Asn Ile Val Leu Ile Ser Tyr Asp Arg Phe Leu Ser Val  
 125 130 135

acc cga gcg gtc tca tac cgg gcc cag cag ggt gac acg cgg cgg gca 726  
 Thr Arg Ala Val Ser Tyr Arg Ala Gln Gln Gly Asp Thr Arg Arg Ala  
 140 145 150

gtg cgg aag atg ctg ctg gtg tgg gtg ctg gcc ttc ctg ctg tac gga 774  
 Val Arg Lys Met Leu Leu Val Trp Val Leu Ala Phe Leu Leu Tyr Gly

155	160	165	
cca gcc atc ctg agc tgg gag tac ctg tcc ggg ggc agc tcc atc ccc 822			
Pro Ala Ile Leu Ser Trp Glu Tyr Leu Ser Gly Gly Ser Ser Ile Pro			
170	175	180	
gag ggc cac tgc tat gcc gag ttc ttc tac aac tgg tac ttc ctc atc 870			
Glu Gly His Cys Tyr Ala Glu Phe Phe Tyr Asn Trp Tyr Phe Leu Ile			
185	190	195	200
acg gct tcc acc ctg gag ttc ttt acg ccc ttc ctc agc gtc acc ttc 918			
Thr Ala Ser Thr Leu Glu Phe Phe Thr Pro Phe Leu Ser Val Thr Phe			
	205	210	215
ttt aac ctc agc atc tac ctg aac atc cag agg cgc acc cgc ctc cgg 966			
Phe Asn Leu Ser Ile Tyr Leu Asn Ile Gln Arg Arg Thr Arg Leu Arg			
	220	225	230
ctg gat ggg gct cga gag gca gcc ggc ccc gag ccc cct ccc gag gcc 1014			
Leu Asp Gly Ala Arg Glu Ala Ala Gly Pro Glu Pro Pro Pro Glu Ala			
235	240	245	
cag ccc tca cca ccc cca ccg cct ggc tgc tgg ggc tgc tgg cag aag 1062			
Gln Pro Ser Pro Pro Pro Pro Pro Gly Cys Trp Gly Cys Trp Gln Lys			
250	255	260	

gcc gtc atc gtg agc atc ttt ggg ctc tgc tgg gcc cca tac acg ctg 1398  
Ala Val Ile Val Ser Ile Phe Gly Leu Cys Trp Ala Pro Tyr Thr Leu

365

370

375

ctg atg atc atc cgg gcc gcc tgc cat ggc cac tgc gtc cct gac tac 1446

Leu Met Ile Ile Arg Ala Ala Cys His Gly His Cys Val Pro Asp Tyr

380

385

390

tgg tac gaa acc tcc ttc tgg ctc ctg tgg gcc aac tgc gct gtc aac 1494

Trp Tyr Glu Thr Ser Phe Trp Leu Leu Trp Ala Asn Ser Ala Val Asn

395

400

405

cct gtc ctc tac cct ctg tgc cac cac agc ttc cgc cgg gcc ttc acc 1542

Pro Val Leu Tyr Pro Leu Cys His His Ser Phe Arg Arg Ala Phe Thr

410

415

420

aag ctg ctc tgc ccc cag aag ctc aaa atc cag ccc cac agc tcc ctg 1590

Lys Leu Leu Cys Pro Gln Lys Leu Lys Ile Gln Pro His Ser Ser Leu

425

430

435

440

gag cac tgc tgg aaa aag atg aag aag aaa aca tgt ctg tgaacttgat 1639

Glu His Cys Trp Lys Lys Met Lys Lys Lys Thr Cys Leu

445

450

gttccctggga tgttttaatca agagagacaa aatigctgag gagctcaggg ctggattggc 1699

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TO350-630-630

gcctctgccc accccgccc tgggctcaca ccagccctgg tggccaagcc tgcgccggcc 1819

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ccaatgtcig tgcacccgig ccacgcgcic tgcattgtcc tctgcctgig cccgctgcgc 1999

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20

<211> 20

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<223> Description of Artificial Sequence: Artificially synthesized primer sequence

tgctctggga caccatcttc

20

$\langle 211 \rangle$  445

&lt;212&gt; PRT

<213> Rattus norvegicus

&lt;400&gt; 25

Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu

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Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala

20 25 30

Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr

35 40 45

Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser

50 55 60

Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp

65 70 75 80

Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu

85 90 95

Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val

100 105 110

Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile

115 120 125

Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala

T0330:0304

130	135	140
Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp		
145	150	155
Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr		
165	170	175
Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe		
180	185	190
Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe		
195	200	205
Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn		
210	215	220
Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly		
225	230	235
Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro		
245	250	255
Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu		
260	265	270



405                      410                      415

Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu

420

425

430

Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys

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aaaaccgggc tgggcgaaga gccggcaaag attaggctca cgagcggggg cccacccgg 240

85                      90                      95

110

125

140

160

175

190

Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe

195	200	205	
-			
acg ccc ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac	973		
Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn			
210	215	220	
atc cag agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc	1021		
Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly			
225	230	235	240
cca gaa ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc	1069		
Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro			
245	250	255	
agc tgc tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg	1117		
Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu			
260	265	270	
cac agg tat ggg gtg ggt gag gca ggc cct ggt gtt gag gct ggg gag	1165		
His Arg Tyr Gly Val Gly Glu Ala Gly Pro Gly Val Glu Ala Gly Glu			
275	280	285	
gct gcc ctc ggg ggt ggc agt ggt gga ggt gct gct gcc tcg ccc acc	1213		
Ala Ala Leu Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Ser Pro Thr			
290	295	300	

tcc agc tct ggc agc tcc tca agg ggc act gag agg cca cgc tca ctc 1261  
 Ser Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu  
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 Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg  
 325 330 335

atg aag atg gtc tcc cag agc atc acc cag cgc ttc cgg ctg tgc cgg 1357  
 Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg  
 340 345 350

gac aag aag gtc gcc aag tgc ctg gcc atc atc gtc agc atc ttt ggc 1405  
 Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly  
 355 360 365

ctc tgc tgg gcg ccg tac acg ctc cta atg atc atc cga gct gct tgc 1453  
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 370 375 380

cat ggc cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt 1501  
 His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu  
 385 390 395 400

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T03350:000000

405

410

415

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Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu

420

425

430

aag gtc cag ccc cac gcc tcc ctg gag cag tgc tgg aag tgagcagctg 1646

Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys

435

440

445

ccccacccctt ctgaggccag gcccttgtac ttgtttgagt gggcagccgg agcgtgggcg 1706

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agtggggtag catggcaggt gggccaagag ccctagittg tggagctaga gtgtgcttgg 1826

tagctctgcc gcacattctc ctccaccaca cagaagagac aatccaggag tcccaggcat 1886

gccttcacct acacacacac acacacacac acacacacac acaccacagt gcagtgccag 1946

tgaigtc

1953

1597 1646 1706 1766 1826 1886 1946 1953